1806

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                        SEQUENCE LISTING
 2
 3        (1)     General Information:
 4
 5          (i) APPLICANT:
 6              (A) NAME: Burkly, Linda C.
 7              (B) STREET: 34 Winthrop Street
 8              (C) CITY: West Newton
 9              (D) STATE: Massachusetts
10              (E) COUNTRY: USA
11              (F) POSTAL CODE (ZIP): 02165
12
13              (A) NAME: Biogen, Inc.
14              (B) STREET: Fourteen Cambridge Center
15              (C) CITY: Cambridge
16              (D) STATE: Massachusetts
17              (E) COUNTRY: USA
18              (F) POSTAL CODE (ZIP): 02142
19
20         (ii) TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES
21
22        (iii) NUMBER OF SEQUENCES: 15
23
24         (iv) COMPUTER READABLE FORM:
25              (A) MEDIUM TYPE: Floppy disk
26              (B) COMPUTER: IBM PC compatible
27              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
29
30          (v) CURRENT APPLICATION DATA:
31              (A) APPLICATION NUMBER: US 000000 (BGP-151CP)
32         (vi) PRIOR APPLICATION DATA:   (B) FILING DATE:
33              (A) APPLICATION NUMBER: PCT/US94/01456
34              (B) FILING DATE: 09-FEB-1994
35        (vii) PRIOR APPLICATION DATA:
36              (A) APPLICATION NUMBER: US 08/029,330
37              (B) FILING DATE: 09-FEB-1993
38
39
40        (2) INFORMATION FOR SEQ ID NO: 1:
41
42          (i) SEQUENCE CHARACTERISTICS:
43              (A) LENGTH: 360 base pairs
44              (B) TYPE: nucleic acid
45              (C) STRANDEDNESS: single
46              (D) TOPOLOGY: linear
```

Corrected Diskette Needed — *Does Not Comply*

Please see, also, back pages. Per 1.824 of Sequence Rules, the computer readable form shall contain a single file on which is recorded a printable copy of the Sequence Listing.

INPUT SET: S15870.raw

```
100
101            (i) SEQUENCE CHARACTERISTICS:
102       (A) LENGTH: 120 amino acids
103       (B) TYPE: amino acid
104       (D) TOPOLOGY: linear
105
106         (ii) MOLECULE TYPE: protein
107         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
108
109    Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
110     1               5                  10                  15
111
112    Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
113        -20-    20              -25-    26              -30-    35
114
115    Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
116     35              40                  45
117
118    Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
119        50                  55                  60
120
121    Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
122     65                  70                  75                  80
123
124    Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
125     85                  90                  95
126
127    Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
128        100                 105                 110
129
130    Gly Thr Thr Val Thr Val Ser Ser
131    115                 120
132
133    (2) INFORMATION FOR SEQ ID NO: 3:
134
135        (i) SEQUENCE CHARACTERISTICS:
136      (A) LENGTH: 318 base pairs
137      (B) TYPE: nucleic acid
138      (C) STRANDEDNESS: single
139      (D) TOPOLOGY: linear
140
141        (ii) MOLECULE TYPE: cDNA
142
143
144        (ix) FEATURE:
145      (A) NAME/KEY: CDS
146      (B) LOCATION: 1..318
147      (D) OTHER INFORMATION:/product= "HP1/2 light
148    chain variable region"
149
150        (ix) FEATURE:
151      (A) NAME/KEY: misc_feature
152      (B) LOCATION: 1
```

[Handwritten margin note:] Please delete all TAB codes between amino acid numbers. They do not process well in the CRF program and cause misalignment. Use space characters instead.

INPUT SET: S15870.raw

```
325     (2) INFORMATION FOR SEQ ID NO: 7:
326
327        (i) SEQUENCE CHARACTERISTICS:
328     (A) LENGTH: 386 base pairs
329     (B) TYPE: nucleic acid
330     (C) STRANDEDNESS: single
331     (D) TOPOLOGY: linear
332
333       (ii) MOLECULE TYPE: cDNA
334
335
336       (ix) FEATURE:
337     (A) NAME/KEY: CDS
338     (B) LOCATION: 1..386
339
340       (ix) FEATURE:
341     (A) NAME/KEY: sig_peptide
342     (B) LOCATION: 1..57
343
344       (ix) FEATURE:
345     (A) NAME/KEY: mat_peptide
346     (B) LOCATION: 58..386
347
348       (ix) FEATURE:
349     (A) NAME/KEY: misc_feature
350     (B) LOCATION: 1
351     (D) OTHER INFORMATION:/note= "pBAG198 insert: VK2
352     (SVMDY) light chain variable region"
353
354
355       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
356
357     ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT        48
358     Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
359     -19             -15             -10                 -5
360
361     GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC        96
362     Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
363        1               5                   10
364
365     AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG       144
366     Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
367        15                  20                  25
368
369     ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG       192
370     Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
371     30                  35                  40                  45
372
373     CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA       240
374     Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
375     50                  55                  60
376
377     TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC       288
```

see next page

INPUT SET: S15870.raw

```
378   Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
379       65              70              75
380
381   CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC        336
382   Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
383   80              85              90
384
385   TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG        384
386   Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
387       95              100             105
388
389   TG
390
391
```

move
386 ⇐ *over*
from
rt./margin

[56]   Carlos et al., 1990, Blood 17:965, "Vascular Cell Adhesion molecule-1 (V

[57]   Miller et al., 1993, J. Exp. Med. 178:211.

[58]   L. Osborn et al., "Direct Expression Cloning of Vascular Cell Adhesion M

[59]   J. Devlin et al., "Random Peptide Libraries: A Source of Specific Protei

[60]   J. Scott and G. Smith, "Searching for Peptide Ligands with an Epitope Li

[61]   U.S. Patent 4,833,092, Geysen, "Method For Determining Mimotopes", issue

The foregoing documents are incorporated herein by reference in their en

SEQUENCE LISTING

sample of large amount of material preceding actual Sequence Listing. Please delete.

CLAIMS:

1. A method for the prevention of insulin dependent (type I) diabet

2. A method according to claim 1, wherein the anti-VLA-4 antibody s

3. A method according to claim 1, wherein the anti-VLA-4 antibody i

4. A method according to claim 1, wherein the anti-VLA-4 antibody i

Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer
program, called Checker, that will aid applicants in identifying
and correcting errors prior to making submissions for compliance
with the Requirements for Patent Applications Containing
Nucleotide Sequence and/or Amino Acid Sequence Disclosures
(sequence rules: 37 CFR 1.821 through 1.825). (Final rules were
published in the *Federal Register* (55 FR 18230) on May 1, 1990,
and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on
May 15, 1990.)

Checker is a DOS-based software program that is intended to
assist users in determining whether errors may be present in the
sequence listings, and is not intended to guarantee that the
submission is error-free.

The most current version of the software will be available via
computer downloading (details below). Copies on diskette are
also available. Updated software versions will not be
automatically mailed out; any updates will be announced in the
PTO *Official Gazette*.

The software can be accessed/requested in the following
locations:
1)   Dial-up access to the Patent and Trademark Office Bulletin
      Board System.
      Phone number: 703-305-8950
      Cost: Free-of-charge
2)   Dial-up access through the Internet. FTP site: ftp.uspto.gov
      Login as "anonymous". Software is in directory /pub/checker
      Cost: Free-of-charge
3)   For diskette copies, telephone requests to 703-306-2600.
      Cost: $25.00

For Further Information Contact: **Arti Shah at 703-308-4212**